Amendment to the Specification:

The paragraph beginning at page 12, line 1 is to be amended to read as follows:

--One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., J. Mol. Biol. 215: 403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). Typically, default program parameters can be used to perform the sequence comparison, although customized parameters can also be used. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix, see for example, Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89,10915 (1989). Conservative substitutions involve substitutions between amino acids in the same class. --